SEQUENCE SEARCH SUMMARY

10/616309

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:20:25 ; Search time 558 Seconds
(without alignments)
10152.675 Million cell updates/sec

Title: US-10-616-309-3
Perfect score: 957
Sequence: 1 atgaagcaactttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	957	100.0	957	12	ADH45224	Adh45224 Enterobac
2	638.8	66.8	1122	3	AAZ98342	Aaz98342 A. thalia
3	556.8	58.2	1041	11	ACH98809	Ach98809 Klebsiell
4	501.4	52.4	1968	5	AAS82067	Aas82067 DNA encod

ADD1 W.O 2100 PF 1100 PD 03

in Ecoli → 3

6610836

4 last only

6610836

	5	257.8	26.9	957	10	ACF71993	Acf71993 Photorhab
	6	257.8	26.9	110000	10	ACF67367_51	Continuation (52 o
	7	257.8	26.9	110000	10	ACF67367_52	Continuation (53 o
	8	257.8	26.9	110000	10	ACF65387_3	Continuation (4 of
	9	191.2	20.0	1020	10	ADF03160	Adf03160 Bacterial
c	10	174.4	18.2	1986	5	AAS92912	Aas92912 DNA encod
c	11	174.4	18.2	2180	5	AAS93271	Aas93271 DNA encod
	12	136.6	14.3	106645	13	ADT05645	Adt05645 Haemophil
	13	136.6	14.3	110000	2	AAT42063_06	Continuation (7 of
	14	100	10.4	100	8	ACD79770	Acd79770 E. coli K
	15	100	10.4	100	8	ACD79771	Acd79771 E. coli K
	16	100	10.4	100	8	ACD79772	Acd79772 E. coli K
c	17	74	7.7	1855	13	ADT05072	Adt05072 Haemophil
c	18	43.2	4.5	2000	8	ADA71938	Ada71938 Rice gene
	19	42.2	4.4	2000	8	ADA71938	Ada71938 Rice gene
c	20	42	4.4	4590	5	AAH24065	Aah24065 Yeast AOD
	21	38	4.0	951	13	ADS60284	Ads60284 Bacterial
c	22	37.8	3.9	763	13	ADS62580	Ads62580 Bacterial
c	23	37.8	3.9	763	13	ADS59814	Ads59814 Bacterial
	24	37.6	3.9	1800	2	AAQ70238	Aaq70238 P. aerugi
	25	37.6	3.9	1800	2	AAQ70237	Aaq70237 P. aerugi
	26	37.6	3.9	1800	3	AAA51920	Aaa51920 P. aerugi
	27	36	3.8	1065	11	ABD14466	Abd14466 Pseudomon
c	28	36	3.8	1308	11	ABD14265	Abd14265 Pseudomon
	29	35.8	3.7	349980	5	AAH68526	Aah68526 C glutami
	30	34.8	3.6	2954	4	AAK91223	Aak91223 Human dig
c	31	34.4	3.6	79256	13	ABD33177	Abd33177 Murine ca
	32	34.2	3.6	421	9	ACH30553	Ach30553 Human tes
	33	34.2	3.6	110000	13	ABD32721_1	Continuation (2 of
c	34	33.6	3.5	168407	13	ABD33266	Abd33266 Murine ca
	35	33.4	3.5	349980	6	ABQ81845	Abq81845 Bifidobac
c	36	33.2	3.5	317	13	ADR60190	Adr60190 Cotton cD
	37	33.2	3.5	1554	13	ADR03666	Adr03666 Aplysia p
c	38	33.2	3.5	1882	2	AAT59768	Aat59768 Rat suppr
c	39	33	3.4	237	5	AAH65905	Aah65905 C glutami
c	40	33	3.4	237	8	ACA00255	Aca00255 C. glutam
c	41	32.8	3.4	1221	4	AAS52633	Aas52633 E. coli D
c	42	32.8	3.4	1221	8	ACA32665	Aca32665 Prokaryot
c	43	32.8	3.4	1221	13	ADT48824	Adt48824 Bacterial
	44	32.6	3.4	467	3	AAC07790	Aac07790 Human sec
	45	32.6	3.4	1813	10	ADF81771	Adf81771 Leukaemia

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:21:35 ; Search time 4168 Seconds
(without alignments)
11125.634 Million cell updates/sec

Title: US-10-616-309-3
Perfect score: 957
Sequence: 1 atgaagcaactttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID			Description
1	957	100.0	957	6	CQ759953	11/94x	0	CQ759953 Sequence App1
2	957	100.0	1661	1	ECU37455	10/95x		U37455 Escherichia knockout
3	957	100.0	3192	1	ECU37089	X		U37089 Escherichia knockout

c	4	957	100.0	12767	1	AE015278	AE015278 Shigella
c	5	957	100.0	29254	1	ECOK12RIII	D64044 Escherichia
c	6	957	100.0	110000	1	U00096_26	Continuation (27 o
c	7	957	100.0	110000	1	U00096_27	Continuation (28 o
c	8	957	100.0	290380	1	AE016987	AE016987 Shigella
c	9	953.8	99.7	10208	1	AE005487	AE005487 Escherich
c	10	953.8	99.7	270365	1	AP002562	AP002562 Escherich
c	11	931.4	97.3	300099	1	AE016764	AE016764 Escherich
c	12	677	70.7	145050	1	AL627275	AL627275 Salmonell
	13	677	70.7	300431	1	AE016835	AE016835 Salmonell
	14	672.2	70.2	13311	1	STAF001386	AF001386 Salmonell
	15	672.2	70.2	13311	6	AX191732	AX191732 Sequence
c	16	672.2	70.2	22108	1	AE008819	AE008819 Salmonell
	17	638.8	66.8	1122	6	BD248394	BD248394 Gene part
	18	556.8	58.2	1041	6	AR387875	AR387875 Sequence
	19	380.8	39.8	4819	1	AY098586	AY098586 Yersinia
	20	355.2	37.1	10886	1	AE013731	AE013731 Yersinia
	21	355.2	37.1	258050	1	AJ414153	AJ414153 Yersinia
	22	355.2	37.1	290294	1	AE017136	AE017136 Yersinia
c	23	353.6	36.9	110000	1	BX936398_34	Continuation (35 o
c	24	319.6	33.4	110000	1	BX950851_36	Continuation (37 o
c	25	257.8	26.9	348505	1	BX571870	BX571870 Photorhab
	26	257.8	26.9	349980	6	AX770909	AX770909 Sequence
	27	228.4	23.9	3545	1	PHRRPOE	L41667 Photobacter
	28	228.4	23.9	3545	1	PHRRPOEA	L41688 Photobacter
c	29	226.8	23.7	349814	1	CR378673	CR378673 Photobact
c	30	202.4	21.1	296650	1	AP005082	AP005082 Vibrio pa
c	31	194.8	20.4	12162	1	AE004316	AE004316 Vibrio ch
	32	191.2	20.0	1020	6	AR378439	AR378439 Sequence
c	33	178.4	18.6	248650	1	AP005341	AP005341 Vibrio vu
	34	167.2	17.5	300732	1	AE016802	AE016802 Vibrio vu
	35	136.6	14.3	10631	1	U32746	U32746 Haemophilus
	36	136.6	14.3	106645	6	CQ873068	CQ873068 Sequence
	37	136.6	14.3	110000	6	BD426631_06	Continuation (7 of
	38	136.6	14.3	110000	6	AR274513_06	Continuation (7 of
	39	136.6	14.3	110000	6	AR541453_06	Continuation (7 of
c	40	122	12.7	11975	1	AE006215	AE006215 Pasteurel
	41	100	10.4	100	6	AX999583	AX999583 Sequence
	42	100	10.4	100	6	AX999584	AX999584 Sequence
	43	100	10.4	100	6	AX999585	AX999585 Sequence
	44	81	8.5	831	1	ECU10148	U10148 Escherichia
	45	79	8.3	110000	1	AE016827_21	Continuation (22 o

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:28:45 ; Search time 207 Seconds
(without alignments)
7564.816 Million cell updates/sec

Title: US-10-616-309-3
Perfect score: 957
Sequence: 1 atgaagcaactttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	556.8	58.2	1041	4	US-09-489-039A-4604	Sequence 4604, Ap
2	191.2	20.0	1020	4	US-09-543-681A-3445	Sequence 3445, Ap
3	136.6	14.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
4	136.6	14.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
5	37.6	3.9	1800	1	US-08-260-202A-10	Sequence 10, Appl
6	37.6	3.9	1800	1	US-08-017-114-10	Sequence 10, Appl
7	37.6	3.9	1800	3	US-08-505-307-10	Sequence 10, Appl
8	37.6	3.9	1800	3	US-09-609-151A-10	Sequence 10, Appl
9	37.6	3.9	1800	5	PCT-US94-02034-10	Sequence 10, Appl
10	36	3.8	1065	4	US-09-252-991A-13070	Sequence 13070, A
c 11	36	3.8	1308	4	US-09-252-991A-12869	Sequence 12869, A

	12	35.2	3.7	601	4	US-09-949-016-193470	Sequence 193470,
c	13	35.2	3.7	268449	4	US-09-949-016-17244	Sequence 17244, A
	14	34.4	3.6	399	4	US-09-621-976-8976	Sequence 8976, Ap
	15	34.2	3.6	254405	4	US-09-949-016-14381	Sequence 14381, A
c	16	33.2	3.5	1882	1	US-08-696-349-1	Sequence 1, Appli
c	17	33.2	3.5	1882	5	PCT-US96-13156-1	Sequence 1, Appli
c	18	32.8	3.4	1788	4	US-09-634-238-184	Sequence 184, App
	19	32.6	3.4	467	4	US-09-513-999C-11865	Sequence 11865, A
	20	32.6	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
	21	32.6	3.4	85122	4	US-09-949-016-14693	Sequence 14693, A
	22	32.6	3.4	119214	4	US-09-949-016-12507	Sequence 12507, A
c	23	32.2	3.4	861	4	US-09-134-000C-507	Sequence 507, App
c	24	32	3.3	505	4	US-09-621-976-15639	Sequence 15639, A
c	25	32	3.3	1152	4	US-09-252-991A-7217	Sequence 7217, Ap
c	26	32	3.3	1389	4	US-09-252-991A-7279	Sequence 7279, Ap
	27	32	3.3	1428	4	US-09-252-991A-7419	Sequence 7419, Ap
c	28	31.8	3.3	1305	4	US-09-248-796A-1639	Sequence 1639, Ap
	29	31.8	3.3	38584	3	US-09-453-702B-50	Sequence 50, Appl
c	30	31.8	3.3	44836	4	US-09-949-016-14867	Sequence 14867, A
c	31	31.6	3.3	370	4	US-09-621-976-15655	Sequence 15655, A
c	32	31.6	3.3	370	4	US-09-621-976-15656	Sequence 15656, A
c	33	31.6	3.3	371	4	US-09-621-976-15654	Sequence 15654, A
c	34	31.6	3.3	373	4	US-09-621-976-15652	Sequence 15652, A
	35	31.6	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	36	31.6	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	37	31.2	3.3	18324	4	US-09-902-540-1196	Sequence 1196, Ap
c	38	31.2	3.3	319608	4	US-09-539-333D-1	Sequence 1, Appli
c	39	31.2	3.3	319608	4	US-09-679-409-1	Sequence 1, Appli
c	40	31	3.2	498	4	US-09-621-976-1174	Sequence 1174, Ap
c	41	31	3.2	2229	4	US-09-196-270-22	Sequence 22, Appl
c	42	31	3.2	2603	4	US-09-620-312D-903	Sequence 903, App
c	43	31	3.2	76269	4	US-09-949-016-14603	Sequence 14603, A
	44	30.8	3.2	1141	4	US-09-806-708B-22	Sequence 22, Appl
c	45	30.8	3.2	5099	4	US-09-887-052-1	Sequence 1, Appli

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:50:01 ; Search time 599 Seconds
(without alignments)
9692.559 Million cell updates/sec

Title: US-10-616-309-3
Perfect score: 957
Sequence: 1 atgaagcaactttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	957	100.0	957	19	US-10-616-309-3 Appl	Sequence 3, Appli
	2	638.8	66.8	1122	16	US-10-342-224-75X	Sequence 75, Appl
	3	136.6	14.3	1830121	17	US-10-329-670-1X	Sequence 1, Appli
	4	136.6	14.3	1830121	18	US-10-158-865-1	Sequence 1, Appli
	5	38	4.0	951	17	US-10-369-493-35958	Sequence 35958, A
c	6	37.8	3.9	763	17	US-10-369-493-35488	Sequence 35488, A
c	7	37.8	3.9	763	17	US-10-369-493-38254	Sequence 38254, A
	8	36.6	3.8	625	14	US-10-123-155-70	Sequence 70, Appl
	9	36.6	3.8	625	15	US-10-146-731-70	Sequence 70, Appl
	10	36.6	3.8	625	15	US-10-140-472-70	Sequence 70, Appl
	11	36.6	3.8	625	15	US-10-141-761-70	Sequence 70, Appl
	12	36.6	3.8	625	16	US-10-142-885-70	Sequence 70, Appl
	13	36.6	3.8	625	16	US-10-158-790-70	Sequence 70, Appl
	14	36.6	3.8	625	17	US-10-137-871-70	Sequence 70, Appl
	15	36.6	3.8	625	17	US-10-140-923-70	Sequence 70, Appl
	16	36.6	3.8	625	17	US-10-141-756-70	Sequence 70, Appl
	17	36.6	3.8	625	17	US-10-141-759-70	Sequence 70, Appl
	18	36.6	3.8	625	17	US-10-140-805-70	Sequence 70, Appl
	19	36.6	3.8	625	17	US-10-140-864-70	Sequence 70, Appl
	20	36.6	3.8	625	17	US-10-142-426-70	Sequence 70, Appl
	21	35.8	3.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
c	22	34.6	3.6	33578	17	US-10-085-117-238	Sequence 238, App
c	23	34.4	3.6	79256	18	US-10-322-281-167	Sequence 167, App
	24	34.2	3.6	421	10	US-09-918-995-17765	Sequence 17765, A
	25	34.2	3.6	400660	18	US-10-388-838-68	Sequence 68, Appl
	26	33.6	3.5	2004	17	US-10-424-599-37007	Sequence 37007, A
c	27	33.6	3.5	168407	18	US-10-322-281-305	Sequence 305, App
	28	33.4	3.5	2256646	18	US-10-470-565-1	Sequence 1, Appli
c	29	33.2	3.5	317	18	US-10-767-795-971	Sequence 971, App
c	30	33	3.4	237	9	US-09-738-626-940	Sequence 940, App
	31	33	3.4	462	17	US-10-242-535A-44051	Sequence 44051, A
	32	33	3.4	462	17	US-10-085-783A-44051	Sequence 44051, A
c	33	33	3.4	576	13	US-10-027-632-321958	Sequence 321958,
c	34	33	3.4	576	17	US-10-027-632-321958	Sequence 321958,
c	35	32.8	3.4	1221	9	US-09-815-242-6270	Sequence 6270, Ap
c	36	32.8	3.4	1221	17	US-10-369-493-47262	Sequence 47262, A
c	37	32.8	3.4	1221	17	US-10-282-122A-20535	Sequence 20535, A
c	38	32.8	3.4	2471	18	US-10-739-930-4858	Sequence 4858, Ap
	39	32.6	3.4	1963	9	US-09-925-300-524	Sequence 524, App
	40	32.6	3.4	5632	14	US-10-198-846-13537	Sequence 13537, A
c	41	32.6	3.4	7047	18	US-10-450-224-1	Sequence 1, Appli
	42	32.6	3.4	358246	17	US-10-292-798-1095	Sequence 1095, Ap
c	43	32.4	3.4	877	17	US-10-282-122A-9278	Sequence 9278, Ap
c	44	32.4	3.4	1242	17	US-10-425-114-5071	Sequence 5071, Ap
	45	32.4	3.4	1494	17	US-10-369-493-35952	Sequence 35952, A

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:27:46 ; Search time 3098 Seconds
(without alignments)
11758.394 Million cell updates/sec

Title: US-10-616-309-3
Perfect score: 957
Sequence: 1 atgaagcaactttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	224.8	23.5	535	9	CL667196	CL667196 PRI0154b_
	2	191.4	20.0	798	9	CL679590	CL679590 PRI0126c_
c	3	119.8	12.5	552	8	AQ990079	AQ990079 Rfc00790
	4	37.6	3.9	928	9	CNS04AQA	AL282187 Tetraodon
	5	36.6	3.8	464	7	CN816649	CN816649 HRO4523_C
	6	36.6	3.8	1289	5	BU305940	BU305940 603612614
	7	36.6	3.8	1378	8	CC260215	CC260215 CH261-1C2
c	8	36.2	3.8	589	5	BQ380762	BQ380762 kk30e04.y

c	9	36.2	3.8	662	5	BQ458073	BQ458073 ko55f03.y
c	10	36.2	3.8	674	5	BQ274578	BQ274578 ko53f02.y
c	11	36.2	3.8	675	5	BQ458055	BQ458055 ko55d05.y
c	12	36.2	3.8	687	5	BQ274580	BQ274580 ko53f06.y
	13	36	3.8	902	6	CA789600	CA789600 AGENCOURT
	14	35.6	3.7	1624	3	CR731608	CR731608 Tetraodon
c	15	35.4	3.7	496	4	BJ305705	BJ305705 BJ305705
	16	35.4	3.7	584	4	BJ322990	BJ322990 BJ322990
	17	35.4	3.7	610	4	BJ311291	BJ311291 BJ311291
c	18	35.4	3.7	649	2	BE442850	BE442850 WHE1107_F
	19	35.4	3.7	679	4	BJ311074	BJ311074 BJ311074
	20	35.2	3.7	313	8	AQ452178	AQ452178 HS_5092_A
c	21	35	3.7	395	9	CNS07H3T	AL610571 Anopheles
	22	35	3.7	484	8	BH377963	BH377963 AG-ND-155
c	23	35	3.7	695	8	BH369286	BH369286 AG-ND-163
c	24	35	3.7	759	7	CK177093	CK177093 EST766413
	25	35	3.7	812	7	CK177094	CK177094 EST766414
c	26	35	3.7	919	9	CNS01JWH	AL147586 Anopheles
	27	34.8	3.6	372	7	CF689180	CF689180 CCAAW76TR
	28	34.8	3.6	649	7	CF682789	CF682789 CCACR84TR
	29	34.8	3.6	662	1	AI392092	AI392092 NCM9C5T3
	30	34.8	3.6	722	7	CO047190	CO047190 Lr_AT1CF_
	31	34.8	3.6	728	7	CF716039	CF716039 CCAHS81TR
	32	34.8	3.6	748	7	CF710464	CF710464 CCAAY96TR
	33	34.8	3.6	765	7	CF714916	CF714916 CCADG32TR
	34	34.8	3.6	774	7	CF722374	CF722374 CCAAO76TR
	35	34.8	3.6	793	7	CF705374	CF705374 CCAGG04TR
	36	34.8	3.6	838	7	CF722152	CF722152 CCAGO08TR
	37	34.8	3.6	858	7	CF694365	CF694365 CCAGV55TR
	38	34.8	3.6	869	7	CF676826	CF676826 CCAHN73TR
c	39	34.6	3.6	295	5	BQ125873	BQ125873 ko46f03.y
c	40	34.6	3.6	328	7	CN243461	CN243461 EST009337
	41	34.6	3.6	331	7	H92696	H92696 yt90d02.r1
c	42	34.6	3.6	342	5	BQ493687	BQ493687 EST02853
c	43	34.6	3.6	359	7	CN242898	CN242898 EST008770
c	44	34.6	3.6	459	5	BQ493062	BQ493062 EST02228
c	45	34.6	3.6	613	4	BG494351	BG494351 602539306